

# Holophyly and associated concepts if the unknown is unclassifiable

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**Abstract.**—In natural sciences, the key criterion for proving the existence of an object (like a physical particle of a previously unknown kind, an atom of a previously unknown element or an organism of a previously unknown species) is its observation and/or observation of traces of the existence of this object (radiation, remains of vital activity etc.). Only objects that meet this criterion can be classified (*e.g.* introduced in the periodic table of elements or described as a species). Single unknown organisms or species can not enter the classification. Despite this, the current system of phylogenetic terms (holo-/monophyly, paraphyly, and polyphyly as they are currently defined) is not adapted to the separation of known and unknown organisms (as well as populations, species, etc.) including ancestral ones. There are longstanding confusion and controversy regarding these “phyletic states”. There seem only two ways in such a situation. The first way is to directly include unknown ancestors in taxa somehow, describe species for them and unavoidably to introduce at least one paraphyletic subtaxon during dividing each taxon. The second way is do not include unknown ancestors in taxa directly and amend the system of concepts and terms. Here the second way was followed and the possible definitions of the main phylogenetic concepts for the views of dealing only with known group members were proposed. Inability to provide a concise definition of holophyly using the existing terms indicates the lack of more basic concepts. These concepts were also proposed here and holophyly was defined using them near the end of the paper. The intersection of four basic “phyly” (*enophyly*, *merophyly*, *kollitophyly*, and *schizophyly*) results in the unambiguous triad of *holophyly*, *paraphyly*, and *schizophyly*. The definitions of the terms in this triad are believed to be unambiguous unlike the widespread definitions of holo-(mono-), para- and “polyphyly”. Here, many terms were defined using others in order not to make the definitions too cumbersome. Nevertheless, the “primary phyly” seem not less useful in phylogenetic discussions than the phyly of the triad. The same is true for the terms *inprestor*, *rendestor*, *ancessure*, *drade* and *skade* as well as for the more precisely defined term *clade*. The first two terms seem to be necessary and important regardless of the views on the classification of unknown organisms.

**Keywords:** *rendestor*; *inprestor*; *enophyletic*; *merophyletic*; *kollitophyletic*; *schizophyletic*; *holophyletic*; *paraphyletic*.

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## INTRODUCTION

The current definitions of holophyly, paraphyly, and polyphyly suggest a direct inclusion of ancestors in taxa. These ancestors are almost always unknown in phylogenetics. Therefore, no one describes them as species and does not include them in taxa. Unknown organisms can not be part of the classification. With this in mind, the triad holo-, para-, and polyphyly can not exist. The difference of holo- and paraphyletic groups from polyphyletic groups is whether the last common ancestor is a member of the group. Since almost always the last common ancestor can not be included in the taxon because this ancestor is unknown, confusion arises. Current phylogenetic discussions require a system of more meaningful and accurate concepts including other definitions of the existing ones.

A remarkable feature of biological systematics and phylogenetics is that known descendants inevitably imply the existence of their ancestors, even if the latter are unknown. But this implication is not enough to “establish the identity” for each of the unknown ancestors. This can be compared to the following analogy from the judiciary. If the existence of some illegal organisation with a leadership management system is proven, then it certainly has a leader. However, this data is not enough to bring

any person to trial. As in the case of unknown ancestors, a “vacancy” is known here, but not a specific identity. Despite all this, non-classification of unknown organisms contradicts the current system of phyletic states and creates confusions in it.

Hennig (1950; 1965; 1966) was probably aware that only known organisms could be classified. At the same time, he considered the probability of finding an ancestor of any group so low that he did not stipulate the inclusion of ancestors in any way in his definitions of phyletic terms. For example, his monophyletic group was defined as all descendants of one ancestor. Ancestors *de facto* were excluded from the groups. This theoretical inaccuracy led to the rapid inclusion of the common ancestor by other authors in the definitions of the three “phyly”. The inclusion was direct and unconditional. This lack of differentiation between known and unknown organisms has led to confusion among taxonomists (see Podani, 2010 for review). Probably, both of the main types of the vision of phylogenetic trees shown by Podani (2010) are not completely correct and the consensus seems possible and necessary (compare Figure 1 in Podani, 2010 and Figure 1 here).

Currently, there is some inconsistency in the phylogenetic practice. The phylogenetic terminology does not specifically stipulate the separation of known and unknown organisms. The definitions are widely used, but users often do not pay attention to unknown organisms. For example, they divide one clade into two subclades, supposedly without a remainder and use the wording “last common ancestor of X” disregarding the unknown organisms, which can be the part of X. If we assume that unknown organisms are not considered members of groups *a priori*, then arises the problem of demarcation of holophyly and paraphyly from enophyly and merophyly respectively (see below). Regardless of the user’s views, the terms “last common ancestor” and “progenitor” are used like there are no unknown organisms at all. Logically, the ancestor/progenitor of the group can not be a member of that group (see Figure 2).

To be consistent we should either to directly include unknown ancestors in taxa somehow, describe species for them and introduce at least one paraphyletic subtaxon per taxon or not to include them directly and amend the terminological system. The differentiation between known and unknown organisms makes it possible to accurately and unambiguously define several phylogenetic terms, to avoid the problem of description of the unknown, and to make the cladistic systematics possible. However, this differentiation makes the changes necessary as well as the amendments in terminology. The revised and supplemented system of concepts with definitions and comments is proposed below.

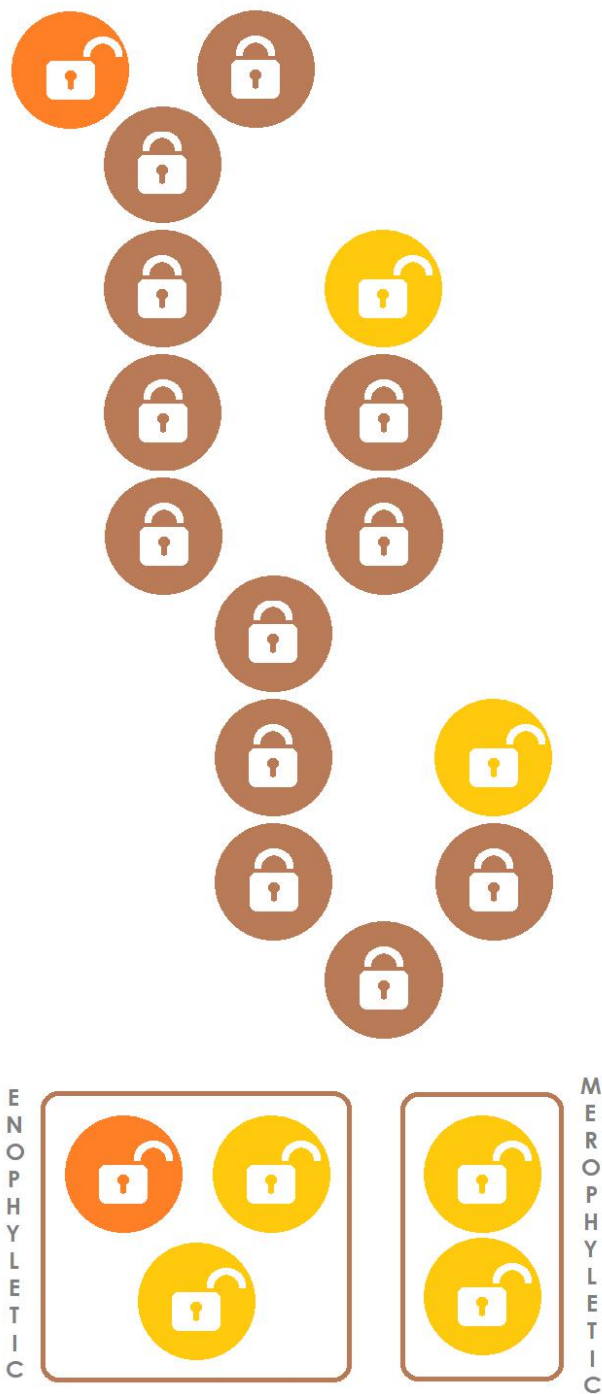
## RESULTS AND DISCUSSION: BASIC CONCEPTS

**PHYLA** (/ˈfaɪlə/; from Greek *φῦλον* [*phylon*] - tribe) — the ancestor plus all its descendants, or the set of a sole member having no descendants.

**ENOPHYLETIC** group (/ɛnə(ʊ)ˈflɪˈlɛtɪk/; from Greek *ενότητα* [*enótita*] - unity) — a set of known organisms, for which at least one phyla exists, all known members of which they are.

**MEROPHYLETIC** group (/mɪrə(ʊ)ˈflɪˈlɛtɪk/; from Greek *μέρος* [*méros*] - part, portion) — a set of known organisms, which have at least one common ancestor, and for which no phyla exists, all known members of which they are.

**POLYPHYLETIC** group (/pɒlɪfɪˈlɪtɪk/; from Greek *πολύς* [*polús*] - many, much) — a set of known organisms, which have no common ancestor; descendants of different ancestors (an exclusively theoretical concept in the present state of knowledge of life in the universe).

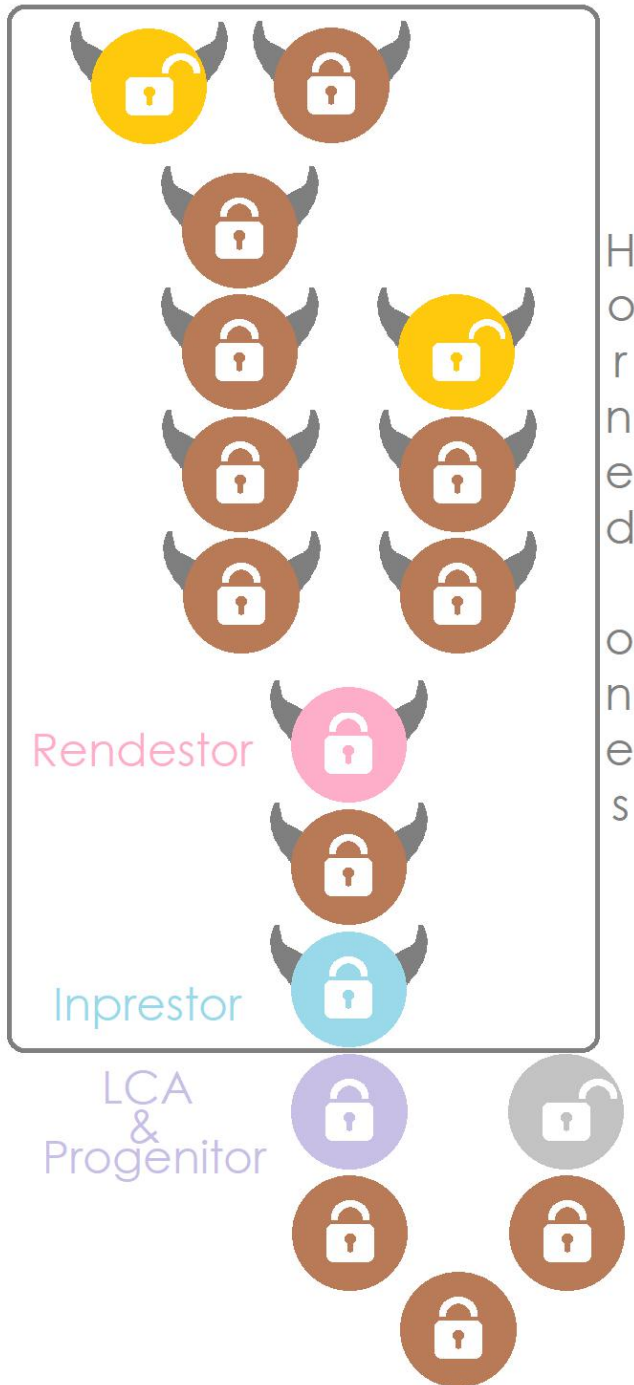


**Figure 1. The tree of ancestor-descendant relationships. Circles with open locks represent known organisms, circles with closed locks represent unknown organisms.**

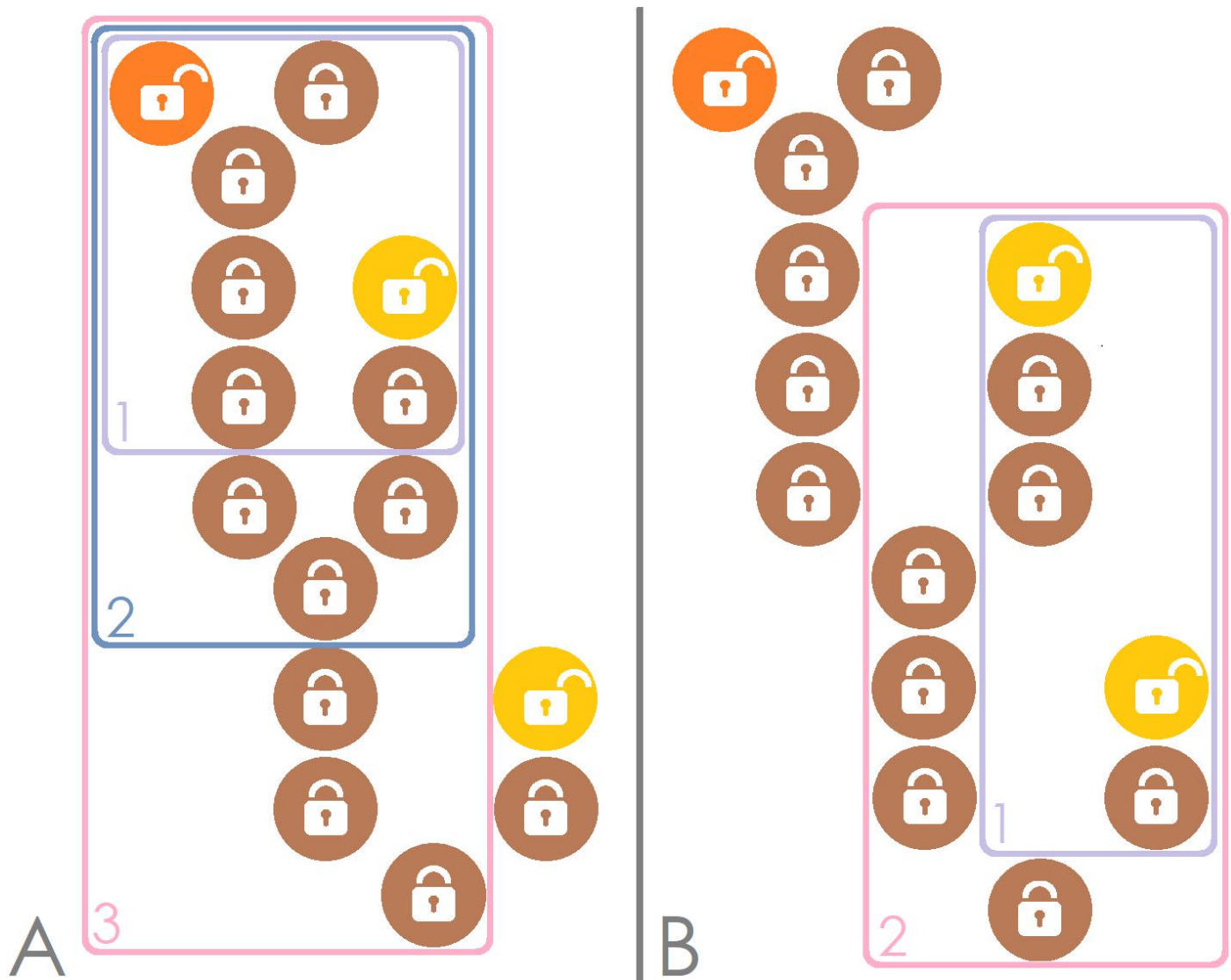
There is the logical and semantical issue with both the wording “*last common ancestor*” and the word “*progenitor*” without adding “*of the known members of the group*”. The progenitor of a group can not be a member of that group. Likewise, an ancestor of a group can not be a member of that group. Therefore, they also should be *unable to be included* in the group (see Figure 2). The phrase “*My granny is the progenitor of my granny, my mother and me*” is not correct. So is this phrase if we replace the word “*ancestor*” with “*progenitor*”. The last common ancestor of Eukaryotes could not have a nucleus. Otherwise, it will be one of the eukaryotes but not their ancestor. The same is with the terms “*concestor*” (simple contraction from “*common ancestor*” coined by Nicky Warren and popularised by Dawkins (2004); see p. 7 in *op. cit.*) and “*cenancestor*” (originally coined by Fitch and Upper (1987)). This issue and the cumbersomeness of the wording “*the last common ancestor of the known members of the X*” as well as un-pronounceability of possible abbreviation LCAKM were reasons for the more short term (*rendestor*) for it. The absence of the concept was the reason for the introduction of *inprestor*.

**INPRESTOR** of the group (/ˈɪnpɹɛstə/ from *in*; Greek *πρώτα* [*próta*] - first; and *ancestor*) — the first in history common ancestor of all known members of the group, which [the ancestor] is able to be included (or is included) in the given group.

**RENDESTOR** of the group (/ˈrɒndɛstə/; portmanteau from Fr. *rendezvous* - a meeting at an agreed time and place - and Eng. *ancestor*) — last common ancestor of all known members of the group except this ancestor itself if this ancestor is known.



**Figure 2.** The tree of ancestor-descendant relationships illustrating the different identities of rendestor, inprestor and last common ancestor (LCA) and progenitor. The grey frame is the borders of the group based on apomorphy of horns.



**Figure 3. Possible diagnostic borders for the same set of two known organisms: enophyletic (A) and merophyletic (B). The groups A1 and B1 are schizophyletic. A2 is holophyletic. A3 and B2 are paraphyletic.**

As the reader could see, the basic criterion, which gives us *eno-* and *merophyly*, are not dealing with unknown organisms, including unknown ancestors. The latter are matter that can not be completely divided into discrete units (*e.g.* could not be divided into a number of species). Although inside it some positions can be distinguished (such as the *rendestor*, the *inprestor* of a feature-based group (*e.g.* apomorphy-gainer), the *inprestor* of a max-clade). As in other cases the lineages of unknown ancestors can not be divided into discrete units and in each given moment of the time appear as solid functional units with the *rendestor/inprestor*, the common term seems highly suitable.

**ANCESSURE** of the group (/ansəs'jʊə/; contraction from *ancestor* and *commissure*) — the *inprestor* of the group (or *rendestor* if there is no single *inprestor*) plus all *inprestor*'s (*rendestor*'s) descendants, which also are ancestors of known members of the given group.

The word “commissure” was not used directly because, for example, the *anceasure* plus all members of the *drade* (see below) do not always represent the *min-clade*, *i.e.* it can contain “a tail” to the *inprestor* when the group has a definition other than that of *min-clade* or simple listing of the

members (see Figures 2, 3, and 4). An *ancessure* is about both known and/or unknown organisms. Using the term *ancessure*, it is possible to define the second basic dichotomy of the phyletic states.

**KOLLITOPHYLETIC** group (/kəlaɪtə(ʊ)fɑɪ'letɪk/; from Greek κολλητός [*kollitós*] - glued) — a group of known organisms, which is able to include all members of its *ancessure* (according to the definition of the group) and no unknown ancestors of known organisms outside the group unless these ancestors are not the sequence of immediate descendants of the *ancessure*.

**SCHIZOPHYLETIC** group (/skɪtsə(ʊ)fɑɪ'letɪk/; from Greek σχίζω [*skhízō*] - split) — a group of known organisms, which is unable to include all members of its *ancessure* (according to the definition of the group) or able to include unknown ancestors of known organisms outside the group if these ancestors are not the sequence of immediate descendants of the *ancessure*.

A kollitophyletic group has the potential to include unknown members of the *ancessure*, but does not include them before they are known. A kollitophyletic group is always able to include the *rendestor* (as it is always the part of the *ancessure*) and has the *inprestor*. Schizophyletic groups are unable to include the *rendestor* and have no single *inprestor*, although their parts have their own *inprestor*s.

Having the two basic phyletic dichotomies it is finally possible to define the duet of phyletic variants emerging at the intersection of kollitophyly with eno- and merophyly (see Figure 4). It is holophyly and paraphyly.

**HOLOPHYLETIC** group (/hɒlə(ʊ)fɑɪ'letɪk/ from Greek ὅλος [*hólos*] - whole) — a kollitophyletic group, the *ancessure* of which did not give rise to any known organism outside the group.

**PARAPHYLETIC** group (/pəɹə(ʊ)fɑɪ'letɪk/; from Greek παρά [*pará*] - beside, near, alongside) — a kollitophyletic group, the *ancessure* of which gave rise to at least one known organism outside the group.

The term *holophyly* was preferred here, because of the number of meanings of the term *monophyly*, both definitional and etymological. Evolutionary taxonomists used it in the same sense as *kollitophyly*. Phylogenetic taxonomists used it in the stricter sense, probably the same as *holophyly*. As there was no differentiation between known and unknown organisms relatively to the phyletic terms before, the additional confusion arose. This confusion allows the term *monophyly* to be treated as a synonym of enophyly or to cover both eno- and merophyly. It is quite attractive to treat *monophyly* in the latter sense (“descendants of one ancestor”) opposed to *polyphyly*, although it extremely reduces the term’s usefulness. Haeckel, who introduced the concepts *monophyly* and *polyphyly* (Haeckel, 1866), also used them as antonyms and, notably, did not reject the possibility of multiple origins of life (*e.g.* Haeckel, 1866 p. 198; 1868 p. 347; 1873 p. 371; 1894 p. 89; see Dayrat, 2003 and Rieppel, 2010 for review). In such views the terms *polyphyly*, as it was defined here, and *monophyly*, as its antonym, were applicable. Despite all this, it is possible to treat *monophyly* as the synonym of *holophyly* (as the latter was defined here).

The distinct entities of enophyletic and holophyletic groups raise the question of to what kind of groups the term *clade* should be ascribed. Although merophyletic groups now are not generally considered clades, there are still three options left of what the clade can be considered (see Figure 4):

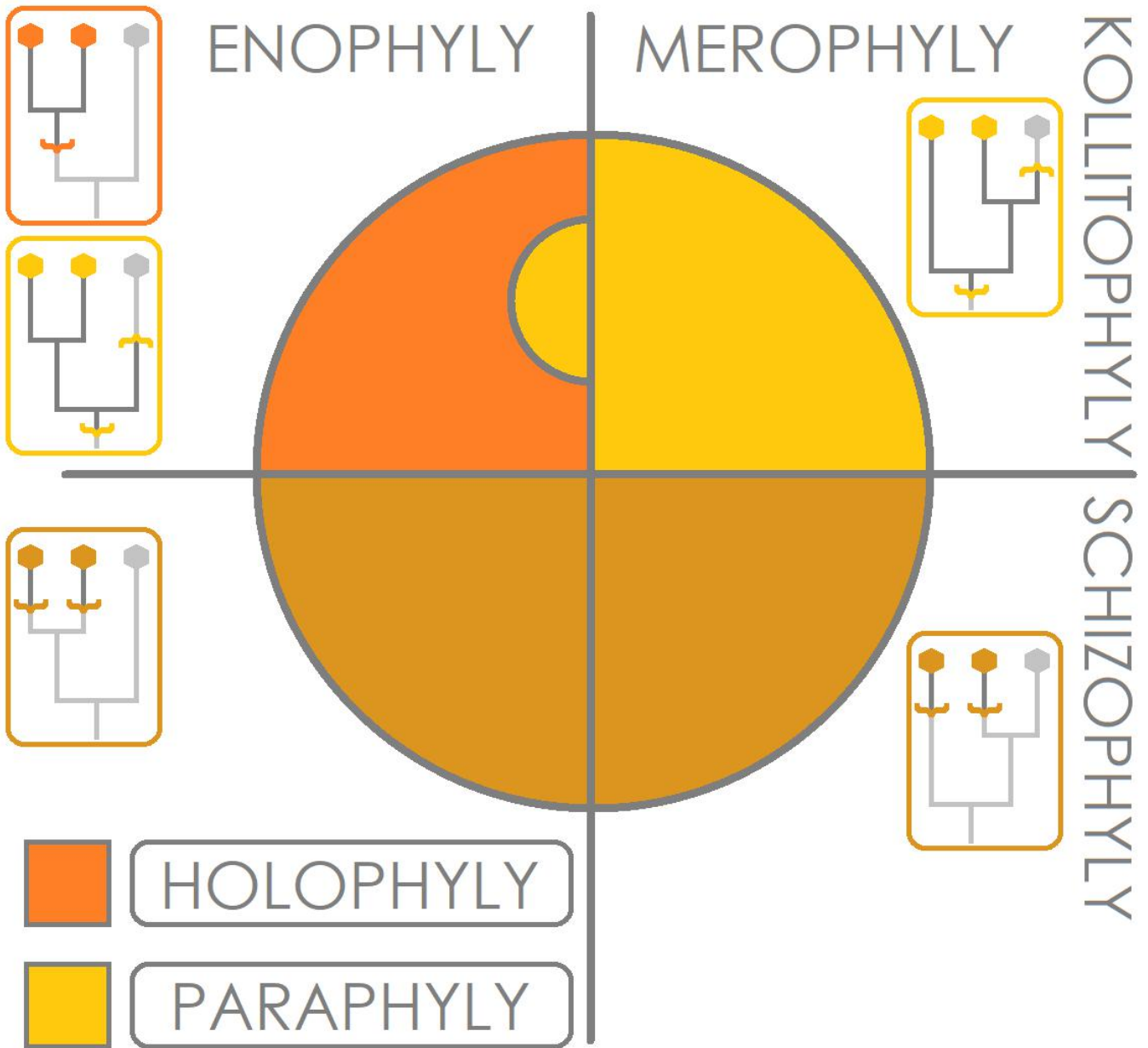


Figure 4. *The diagram of the relationships of “phyly” among themselves. Coloured hexagons represent known group members. Grey hexagons represent the known organisms outside the group. The groups: on all three trees on the left are enophyletic; on all two trees on the right are merophyletic; on all three trees above are kollitophyletic; on all two trees below are schizophyletic. The colour of the hexagons and borders around each tree matches the colour of the segment of the vertical half of the diagram.*

1) an enophyletic group, 2) a kollito-enophyletic group or 3) a holophyletic group. As the etymology of the term *clade* (from Greek κλάδος [kládos] - shoot, branch) minds the inclusion of the ancessure and no breaks in the branch, here the term *clade* was applied only to holophyletic groups as they were defined here.

Such an interpretation of the term *clade* borns the issue with the groups formed by a simple listing of their members or subgroups. Such groups are unable to include their entire ancessures. For example, the wordings “Sar+Telonemia clade” or “Telonemia formed the clade with Sar” or “TSAR clade” will not be correct since the ancessure is not fully included here (see Strassert *et al.*, 2019 for the phylogeny). For such purposes, the short term for “*enophyletic group*” seems needed.

**DRADE** /dɹeɪd/ — an enophyletic group (from the two first letters of the semantic core in L. *polydrupa* - the type of fruit to which raspberries belong, bramble fruit; the type of aggregate fruit easily separable from the receptacle) and the ending *-ade*, like in the terms *grade* and *clade*).

**CLADE** /kleɪd/ — a holophyletic group (from Greek κλάδος [*kládos*] - shoot, branch).

The short term for paraphyletic groups also seems necessary there. The term [evolutionary] *grade* does not mean “a paraphyletic group”. Grades can also be holophyletic and schizophyletic as these terms were defined here (see Huxley 1957; 1958; 1959).

**SKADE** /skeɪd/ — a paraphyletic group (from Greek σκαλών [*skalón*] - flight of stairs).

## CONCLUSIONS

- 1) Every two currently known organisms are descendants of one ancestor. Therefore, true polyphyly does not exist in the current scientific reality.
- 2) Regardless of the likelihood of knowing each specific ancestor, a good system of concepts should be designed for the case when ancestors are found. The likelihood of this is very high near the terminals of the Tree of Life. However, the inclusion of unknown organisms (including unknown ancestors) can not be direct and immediate.
- 3) A group having the same composition may have different “phyletic state”, depending on how this group is defined. Only eno- or merophyly reflects the composition of the group. All other “phyletic states” described here depend on the definition of each specific group.
- 4) *Rendestor* is a short and correct term for what is now misleadingly and confusingly called a last common ancestor, almost always without adding “of the known members of X”.
- 5) In discussions about the origin of a group (for example, about eukaryogenesis), we are talking primarily about the *inprestor* of this group. This makes the term highly desirable.
- 6) *Ancessures* of groups is a hitherto unnamed component of phylogenetic trees, usually shown simply by lines. Members of an *ancessure* are usually unable to be included in taxa but should be able to be included in that taxa, which are considered holophyletic or paraphyletic (i.e. in kollitophyletic taxa).
- 7) To be holophyletic or paraphyletic, the group must be able to include the entire *ancessure* (see also Kwok (2010), who used the terms “connected group” and “disconnected group”, although he does not distinguish between known and unknown organisms). In other cases, we can only talk about *enophyly* or *merophyly*.
- 8) The demarcation between *enophyly* and *holophyly* is the Achilles’ heel of existing terminological systems.
- 9) The difference of holophyletic and paraphyletic groups from schizophyletic groups is the ability to include the entire *ancessure*.
- 10) The difference of holophyletic groups from paraphyletic groups is whether the *ancessure* of the group gave rise to any known organism outside the group.



11) Definitions of the term *clade* that do not use the separation of known and unknown organisms **do not allow any clade to be completely divided into subclades**—at least the *rendestor* will remain. This has been emphasised, for example, by Cavalier-Smith (1998 p. 211). Such definitions of the *clade* create problems in cladistic systematics. Cladistic systematics is the drive to constantly reduce non-holophyletic groups to only unknown organisms. However, such a definition of the clade (like the one given here for the phyla) is widespread and adopted, for example, by the PhyloCode (Article 2.1). Regardless of how acceptable we think paraphyletic groups are, cladistics is possible only in the views adopted here and paraphyletic groups can be reduced to cases with known ancestors.

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## ORIGINS OF THE TERMS

The number of terms used here was introduced by other authors with the different definitions and/or application. The terms *monophyly/monophyletic* and *polyphyly/polyphyletic* originated from Haeckel (1866). The terms *paraphyly/paraphyletic* originated from Hennig (1965). The terms *holophyly/holophyletic* originated from Ashlock (1971). The terms *merophyly/merophyletic* originated from Bernardi (1981). The term *clade* originated from Cuénot (1940).

The terms *enophyly/enophyletic*, *kollitophyly/kollitophyletic*, *schizophyly/schizophyletic*, *drade*, *skade*, *inprestor*, *rendestor*, and *ancessure* are believed by the author to be new.

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## DECLARATIONS OF INTEREST

None.

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## REFERENCES

Ashlock, P. D. (1971). Monophyly and Associated Terms, *Systematic Biology*, 20(1), 63–69.

[doi.org/10.1093/sysbio/20.1.63](https://doi.org/10.1093/sysbio/20.1.63)

Bernardi, N. (1981). Parentesco filogenético, grupo monofilético e conceitos correlatos: novas definições. *Revista Brasileira de Entomologia*, 25(4), 323–326.

Cavalier-Smith, T. (1998). A revised six-kingdom system of life. *Biological Reviews*, 73, 203–266.

[doi.org/10.1111/j.1469-185X.1998.tb00030.x](https://doi.org/10.1111/j.1469-185X.1998.tb00030.x)

Cuénot, L. (1940). Remarques sur un essai d'arbre généalogique du règne animal. *Comptes rendus hebdomadaires des séances de l'Académie des sciences*, 210, 23–27.

[gallica.bnf.fr/ark:/12148/bpt6k31623/f24.item](https://gallica.bnf.fr/ark:/12148/bpt6k31623/f24.item)

Dawkins, R. (2004). *The Ancestor's Tale: A Pilgrimage to the Dawn of Life*. Boston: Houghton Mifflin.

Dayrat, B. (2003). The Roots of Phylogeny: How Did Haeckel Build His Trees? *Systematic Biology*, 52(4), 515–527. doi.org/10.1080/10635150390218277

Fitch, W. M. & Upper, K. (1987). The phylogeny of tRNA sequences provides evidence for ambiguity reduction in the origin of the genetic code. *Cold Spring Harbor Symposia on Quantitative Biology*, 52, 759–767. doi.org/10.1101/sqb.1987.052.01.085

Haeckel, E. (1866). *Generelle Morphologie der Organismen: Allgemeine Grundzüge der organischen Formen-Wissenschaft, mechanisch begründet durch die von Charles Darwin reformirte Descendenz-Theorie*. Erster Band: *Allgemeine Anatomie der Organismen*. Verlag von G. Reimer, Berlin. doi.org/10.5962/bhl.title.3953

Haeckel, E. (1868). *Natürliche Schöpfungsgeschichte. Gemeinverständliche wissenschaftliche Vorträge über die Entwicklungslehre im Allgemeinen und diejenige von Darwin, Goethe und Lamarck, im Besonderen über die Anwendung derselben auf den Ursprung des Menschen und andere damit zusammenhängende Grundfragen der Naturwissenschaft*. Berlin. Verlag von Georg Reimer.

Haeckel, E. (1873). *Natürliche Schöpfungsgeschichte. Gemeinverständliche wissenschaftliche Vorträge über die Entwicklungslehre im Allgemeinen und diejenige von Darwin, Goethe und Lamarck und Besonderen*. Vierte verbesserte Auflage. Berlin, Verlag von Georg Reimer. doi.org/10.5962/bhl.title.15259

Haeckel, E. (1894). *Systematische Phylogenie. Entwurf eines Natürlichen Systems der Organismen auf Grund ihrer Stammesgeschichte*. Erster Theil: *Systematische Phylogenie der Protisten und Pflanzen*. Berlin, Verlag von Georg Reimer. doi.org/10.5962/bhl.title.3947

Hennig, W. (1950). *Grundzüge einer Theorie der Phylogenetischen Systematik*. Deutscher Zentralverlag, Berlin.

Hennig, W. (1965). Phylogenetic systematics. *Annual Review of Entomology*, 10, 97–116. doi.org/10.1146/annurev.en.10.010165.000525

Hennig, W. (1966). *Phylogenetic systematics*. University of Illinois Press, Urbana.

Huxley, J. S. (1957). The three types of evolutionary process. *Nature*, 180(4584), 454–455. doi.org/10.1038/2F180454a0

Huxley, J. S. (1958). *Evolutionary processes and taxonomy with special reference to grades*. pp. 21–39, in Hedberg, O. (ed). *Systematics Today*. Uppsala Universitets Arsskrift, Sweden.

Huxley, J. S. (1959). *Clades and grades*. pp. 21–22, in Cain, A. J. (ed). *Function and Taxonomic Importance*. The Systematics Association, London.

Kwok, R. B. H. (2010). Phylogeny, genealogy and the Linnaean hierarchy: a logical analysis. *Journal of Mathematical Biology*, 63(1), 73–108. doi.org/10.1007/s00285-010-0364-6

Podani, J. (2010). Monophyly and paraphyly: A discourse without end? *Taxon*, 59(4), 1011–1015. doi.org/10.2307/20773972

de Queiroz, K. & Cantino, P. D. (2020). *International Code of Phylogenetic Nomenclature (PhyloCode)*. CRS Press. doi.org/10.1201/9780429446320

Rieppel, O. (2010). Ernst Haeckel (1834-1919) and the monophyly of life. *Journal of Zoological Systematics and Evolutionary Research*, 49(1), 1–5. doi.org/10.1111/j.1439-0469.2010.00580.x

Strassert, J. F. H., Jamy, M., Mylnikov, A. P., Tikhonenkov, D. V. & Burki, F. (2019). New Phylogenomic Analysis of the Enigmatic Phylum Telonemia Further Resolves the Eukaryote Tree of Life. *Molecular Biology & Evolution*, 36(4), 757–765. doi.org/10.1093/molbev/msz012

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